In the Specification:

Please amend the specification as shown:

Please delete the paragraphs on page 10, lines 23-31 and replace them with the following paragraphs:

FIG. 1: Amino acid sequences of the hGH high affinity site antagonist framework scyllatoxin, the hGH antagonists SCY01, SCY02, SCY03 and their alignment with the hGH sequence. Disulfide linkages are indicated by lines connecting cysteines. **Figure discloses SEQ ID NOS: 1-6, respectively, in order of appearance.**

FIG. 2: Amino acid sequences for the hGH agonist framework VIB, the engineered molecule VIB01 and the alignment with the hGH sequence. Disulfide linkages are indicated by lines connecting cysteines. **Figure discloses SEQ ID NOS: 7-10, respectively, in order of appearance.**

Please delete the paragraph on page 11, lines 17-21 and replace it with the following paragraph:

FIG. 9: Amino acid sequence for the low affinity site hGH anatagonist framework ZDC and the engineered hGH anatagonist ZDC05 and the aligned hGH sequence. Disulfide linkages are indicated by lines connecting cysteines. **Figure discloses SEQ ID NOS: 11-14, respectively, in order of appearance.**

Please delete the paragraph on page 11, lines 23-26 and replace it with the following paragraph:

FIG. 11: Amino acid sequences of the hGH agonist framework ERP, the engineered molecules ERP01, ERP02, ERP03 and their alignment with the hGH sequence. Disulfide linkages are indicated by lines connecting cysteines. **Figure discloses SEQ ID NOS: 15-20, respectively, in order of appearance.**

Please delete the paragraph on page 12, lines 4-7 and replace it with the following paragraph:

FIG. 14: Amino acid sequences of the CD4 frameworks PTA and SCY, the engineered molecules PTA CD4, and SCY CD4 and the alignment with the CD4 sequence. Disulfide linkages are indicated by lines connecting cysteines. **Figure discloses SEQ ID NOS: 21-25, respectively, in order of appearance.**

Please delete the paragraph on page 36, line 23 to page 37, line 5 and replace it with the following paragraph:

The pure reduced peptides SCY 01-03 were folded using 0.1M solution of NH_4HCO_3 stirred overnight at RT at a peptide concentration of ~0.3 μM per ml monitored by HPLC and mass spectrometry. The folded peptide was isolated by preparative HPLC and mass spectrometry. The folded peptide was isolated by preparative HPLC. The correct disulphide connectivity for SCY01 was determined by full structure analysis by NMR. Folding methods using oxidized and reduced glutathione in a ratio of 100:10:1 GSH:GSSG: peptide **(GSSG disclosed as SEQ ID NO: 26)** and published methods using 5mM GSSG **(SEQ ID NO: 26)** to 0.5mM GSH in $NaPO_4$ buffer pH 7.4 was carried out it give identically folded material. After folding the pure peptide an equivalent yield of peptide was obtained by folding the crude peptide in exactly the same manner. The oxidation of SCY13 was complicated by the

Fm group attached to the Glu. SCY13 was oxidised using a 30% TFE solution in the presence of 5mM GSSG **(SEQ ID NO: 26)** to 0.5 mM GSH in $NAPO_4$ buffer pH 7.4.

Please delete the paragraph on page 42, lines 11-15 and replace it with the following paragraph:

The peptide was dissolved at a low concentration in cold water to which was added triflouroethanol to 30%. This was cooled at 4°C for two hours before oxidised and reduced glutathione was added (10:100:1/GSSG:GSH:peptide**; GSSG disclosed as SEQ ID NO: 26**) then 1M NH_4HCO_3 was added to give a 0.1M solution at pH 8.1. The oxidised peptides were isolated HPLC.

Please delete the paragraph on page 45, lines 8-10 and replace it with the following paragraph:

The SCY CD4 molecule was oxidised using 5 mM GSSG **(SEQ ID NO: 26)** to 0.5 mM GSH in NaPO4 buffer pH 7.4. The oxidised peptide was purified by HPLC.